



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/814,760
Source: IFL40
Date Processed by STIC: 9/24/04

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

~~TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER~~
~~VERSION 4.2 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND~~
~~TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:~~

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box-1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 06/05/04):
U.S. Patent and Trademark Office, 220 20th Street S., Customer Window, Mail Stop Sequence, Crystal Plaza Two, Lobby, Room 1B03, Arlington, VA 22202

Revised 05/17/04

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 10/8/4,760

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 ☒ Wrapped Nucleics
1 ☒ Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor **after** creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 ☒ Invalid Line Length The rules require that a line **not exceed** 72 characters in length. This includes white spaces.
- 3 ☐ Misaligned Amino
3 ☐ Numbering The numbering under each 5th amino acid is misaligned. Do **not** use tab codes between numbers; use **space characters**, instead.
- 4 ☒ Non-ASCII The submitted file was **not** saved in ASCII(DOS) text, as **required** by the Sequence Rules. Please **ensure your subsequent submission is saved in ASCII text**.
- 5 ☐ Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the **maximum** number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 ☐ PatentIn 2.0
6 ☐ "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**
- 7 ☐ Skipped Sequences Sequence(s) missing. If intentional, please insert the following lines for **each** skipped sequence:
(OLD RULES) (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to **include** the skipped sequences.
- 8 ☐ Skipped Sequences Sequence(s) missing. If intentional, please insert the following lines for **each** skipped sequence.
(NEW RULES) <210> sequence id number
<400> sequence id number
000
- 9 ☐ Use of n's or Xaa's Use of n's and/or Xaa's have been detected in the Sequence Listing.
(NEW RULES) Per 1.823 of Sequence Rules, use of <220>-<223> is **MANDATORY** if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 ☐ Invalid <213> Per 1.823 of Sequence Rules, the only **valid** <213> responses are: Unknown, Artificial Sequence, or
10 ☐ Response scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or
is Artificial Sequence
- 11 ☐ Use of <220> Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is **MANDATORY** if <213> "Organism" response is "Artificial Sequence" or
"Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 ☐ PatentIn 2.0 Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file,
12 ☐ "bug" resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence
listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 ☐ Misuse of n/Xaa "n" can **only** represent a single nucleotide; "Xaa" can **only** represent a single amino acid

Please consult Sequence Rules
for valid format.



Also, see item 4 on Error Summary sheet, IFWO
and item 2 on Error Summary sheet

delete
Extra <1107's;
show <1107
only once

RAW SEQUENCE LISTING

DATE: 09/24/2004

PATENT APPLICATION: US/10/814,760

TIME: 10:49:45

Input Set : N:\LMOORE\PTO.LM.txt

Output Set: N:\CRF4\09242004\J814760.raw

pp 2-4
Does Not Comply
Corrected Diskette Needed

8 <110> APPLICANT: Buchanan, F.
W--> ~~4 <110>~~ APPLICANT: Thue, T.D.
W--> ~~5 <110>~~ APPLICANT: Winkelman-Sim, D.
W--> 6 <120> TITLE OF INVENTION: CRH and POMC Effects on Animal Growth
W--> 7 <130> FILE REFERENCE: 1696-04-02
C--> 8 <140> CURRENT APPLICATION NUMBER: US/10/814,760
C--> 8 <141> CURRENT FILING DATE: 2004-03-31
E--> 9 <160> NUMBER OF SEQ ID NOS: Number of SEQ ID NOS: 9
10 <170> SOFTWARE: Microsoft Office 2004; Windows XP Professional O/S.

ERRORED SEQUENCES

E--> 13 <210> SEQ ID NO: SEQ ID NO: 1
14 <211> LENGTH: LENGTH: 584 base pairs
E--> 15 <212> TYPE: TYPE: DNA
16 <213> ORGANISM: ORGANISM: Bos taurus
W--> 17 <220> FEATURE: FEATURE: SNPs present at nucleotides 22 ("CRH4"), 145 ("CRH45") and 240
W--> 18 ("CRH77").
19 <223> OTHER INFORMATION: OTHER INFORMATION: GenBank Accession AF340152
E--> 21 <400> SEQUENCE: SEQUENCE 1
W--> 22 1 cgcccgctaa aatgcgactg ccgctgctcg tgcctgtggg cgtcctgctg gtggctctgc
W--> 23 61 tgccctcccc gccatgcagg gccctctca gccgggggcc catcccggt gccgcgagg
W--> 24 121 catcacagca cccccagccc ctgagtttct tccagccgcc gccgcagccc caggaacccc
W--> 25 181 aggtctctgcc caccctactc cgtgttgggg aggaatactt cctccgctcg ggtaacctcg
W--> 26 241 atgagaccgc ggctgtctcs ctctctcccg ccgcctcgcc tctcgccagc agaagcagca
W--> 27 301 gtcgccttct tccggacaag gtggccgcc aacttttccg agcgtgctg cagccccggc
W--> 28 361 gccattcga cagcccagcg ggcccgcg aacgcggcac ggagaacgcc ctgggcagcc
W--> 29 421 gccaggaggc gccggccgcc aggaagaggc gatcccagga acctcccatc tccctggatc
W--> 30 481 tcaccttcca cctctctcga gaagtcttgg aatgaccaa ggccgatcag ttagcacagc
E--> 31 541 aagctcatar caayaggaaa ctgttggaac ttgctgggaa atga
E--> 35 <210> SEQ ID NO: SEQ ID NO: 2
36 <211> LENGTH: LENGTH: 1002 base pairs
E--> 37 <212> TYPE: TYPE: DNA
38 <213> ORGANISM: ORGANISM: Bos taurus
W--> 39 <220> FEATURE: FEATURE: SNP at position 254
40 <223> OTHER INFORMATION: OTHER INFORMATION: GenBank Accession J00021
E--> 42 <400> SEQUENCE: SEQUENCE 2
W--> 43 1 gcggaggagg tggaaggctc aggcggcgcg cttgaggggc ggggtgaacgc cgcggcctgg
W--> 44 61 agtggggcgg gctgacgcg ctctgcccgt ctccgcaggc gtgcatccgg gctgcaagc
W--> 45 121 ccgacctctc ccgcgagacg ccggtgttcc ccggcaacgg cgatgagcag ccgtgactg
W--> 46 181 agaacccccg gaagtacgtc atgggccatt tccgctggga ccgcttcggc cgtcgggaatg
W--> 47 241 gtagcagcag cagcggagtt gggggcgcg cccagaagcg cgaggaggaa gtggcggtgg

see
P.2
for explanation
of global
error

10/8/14, 760

2

Sequence Listing

<110> Buchanan, F.

<110> Thue, T.D.

<110> Winkelman-Sim, D.

<120> CRH and POMC Effects on Animal Growth

<130> 1696-04-02

<141> March 31, 2004

<160> Number of SEQ ID NOS: 9

<170> Microsoft Office 2004; Windows XP Professional O/S.

<140> 10/8/14, 760 <insert

2004-03-31 use this format for dates

do not insert alphabetical headings

<210> SEQ ID NO: 1

<211> LENGTH: 584 base pairs

<212> TYPE: DNA

<213> ORGANISM: Bos taurus

<220> FEATURE: SNPs present at nucleotides 22 ("CRH4"), 145 ("CRH45") and 240 ("CRH77").

<223> OTHER INFORMATION: GenBank Accession AF340152

<400> SEQUENCE 1

cgcccgctaa aatgcgactg ccgctgctcg tgtccgtggg cgtcctgctg gtggctctgc
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<600>

10/8/4,760 3

<210> ~~SEQ ID NO:~~ 3

<211> ~~LENGTH:~~ 1809 base pairs

<212> ~~TYPE:~~ DNA

<213> ~~ORGANISM:~~ Bos taurus

<223> ~~FEATURE:~~ SNP at position 1069

<223> ~~OTHER INFORMATION:~~ (Genbank Accession No. AF265221)

<400> ~~SEQUENCE~~ 3

1 cagcctaaga ttccaagt atgctgacca gagccacact tgaaagagac tgaaaacttc

6 ctttcagct cggagcatg ggacatttat tcaagcagg catgccactc tccgcgcct

121 aactttcgtt tggggcaagt caagactgga gaaaggtgct gaggtcgcca gatccaggag

60 ← insert
120 ← insert
180 ←

(partial listing of sequence 3)

insert

<300> ← no response

<308> ←

<309> ← insert response

The above is a

sample of global error

10/8/4,760 4

2207 <210> ~~SEQ ID NO:~~ 6
2237 <211> ~~LENGTH:~~ 21
<212> ~~TYPE:~~ DNA
↑ <213> ~~ORGANISM:~~ Bos taurus insert <2207 above <2237>
<223> ~~OTHER INFORMATION:~~ Forward primer for DNA amplification of sequences
within SEQ ID NO: 2.
use
forward
packet
-1 <400> ~~SEQUENCE:~~ 6
cgtgcatccg ggctgcaag c 21

The above is another sample of global error.

Please see sample Sequence Listing
(attached) for valid format.

<110> Smith, John; Smithgene Inc.

<120> Example of a Sequence Listing

<130> 01-00001

<140> PCT/EP98/00001
<141> 1998-12-31

<150> US 08/999,999
<151> 1997-10-15

<160> 4

<170> PatentIn version 2.0

<210> 1
<211> 389
<212> DNA
<213> Paramecium sp.

<220>
<221> CDS
<222> (279)...(389)

<300>
<301> Doe, Richard
<302> Isolation and Characterization of a Gene Encoding a
Protease from Paramecium sp.
<303> Journal of Genes
<304> 1
<305> 4
<306> 1-7
<307> 1988-06-31
<308> 123456
<309> 1988-06-31

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aggagagagtg tcttgaccct cctctgcctt tgcagcttca caggcaggca ggcaggcagc 120
tgatgtggca attgctggca gtgccacagg cttttcagcc aggcttaggg tgggttcgcg 180
cgcggcgcgg cgccccctct cgcgctctc tcgcgctct ctctcgctct cctctcgctc 240

Consult this

ggacctgatt	agggtgagcag	gaggaggggg	cagtttagc	atg Met 1	gtt Val	tca Ser	atg Met	ttc Phe 5	agc Ser	296						
ttg Leu	tct Ser	ttc Phe	aaa Lys 10	tgg Trp	cct Pro	gga Gly	ttt Phe	tgt Cys 15	ttg Leu	ttt Phe	gtt Val	tgt Cys	ttg Leu 20	ttc Phe	caa Gln	344
tgt Cys	ccc Pro	aaa Lys 25	gtc Val	ctc Leu	ccc Pro	tgt Cys	cac His 30	tca Ser	tca Ser	ctg Leu	cag Gln	ccg Pro 35	aat Asn	ctt Leu	389	

<210> 2
<211> 37
<212> PRT
<213> Paramecium sp.

<400> 2	Met 1	Val	Ser	Met	Phe 5	Ser	Leu	Ser	Phe	Lys 10	Trp	Pro	Gly	Phe	Cys 15	Leu
	Phe	Val	Cys	Leu 20	Phe	Gln	Cys	Pro	Lys 25	Val	Leu	Pro	Cys	His 30	Ser	Ser
	Leu	Gln	Pro 35	Asn	Leu											

<210> 3
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Designed peptide based on size and polarity to act as a linker between the alpha and beta chains of Protein XYZ.

<400> 3	Met 1	Val	Asn	Leu	Glu 5	Pro	Met	His	Thr	Glu 10	Ile
---------	----------	-----	-----	-----	----------	-----	-----	-----	-----	-----------	-----

<210> 4
<400> 4
000

[Annex VIII follows]